

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

```
1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC
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Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

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1 gccggcctccagcagcgggcgcggcgggcgcgagcacgacccactctcctgcggccgcg
61 ggtggagcagcgcgagccgcctcgctgagccggccggggcgaggatgagttgcggc
121 cccgcggcagcgcgccagcatggggaggagcgcgcggcactgccctcgagaactggcgct
181 ccggtgaagttaggcgcgcggccggtccgcctccccaagccggttcgcacccgcggccgcg
1 M A G S G A W K R L K S M L R K
241 tcagcctctgccATGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGAAAGGCCTGTTAACGGGGCGCACCCGACCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATAACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATT
177 H R L E V L S A M I S V L L V Y I L M G
781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
```

Figure 2A continued

197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCACTCTGGTCACCGTCACTCCCATTCCTGCCTTCAAATTCCCCTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTACGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTGAGAGTTCTAGTCCCTAAAtttatgtattttgggaa
1561 ctccctgccttatttctcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtacgtgtcttaaaggaagcatc
1861 aagaattcaatatatttgcatTTAAAAatactttttaaggccattttatattaagccagtg
1921 tggaaaactgaattttttttattatgtataataatctcgacacccagcttctggaattgc
1981 tgctttctttttacagaaattactacccaacagatttcaggaagtactagtagttatccc
2041 aaaagtggaaataagcatgtattcctaagtgttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgattatactttataaacaaccttttccagatgctacagggttt
2161 tgaatctcaaagttaacatttttcattatttgaatcttagaaccaaatctttatttatt
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag
2281 ttagtcttaaaactcaaattactatatgatgattttaaacaataaaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCACTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATTCCTTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
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Figure 2B continued

1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAAGATTACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAAGTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCCTCAAATCCCCTACCAGAGGTTCTGGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTGAAT
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Figure 2C continued

341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt
1321 cactttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtctctgttttaaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID Nos: 2569, 2571 & 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
v.1	GGCGGCCTCAGCAG	CGGCGCGCGGGCGG	CGAGACGACCCAC	TCTCCTGCGGCGCGG	GGTGGAGCAGCGCGA	GGCGGCCTCGCTGAG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
91	105	106	120	121	135	136	150	151	165	166	180
v.1	CGGCGCGGGGCGGG	GAGATCAGTTGCGC	CCGCGCGCAGCGCC	CAGGATGGGAGGGA	CGCGCGCACGTGCC	TCGAGAACTGGCGCT					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
181	195	196	210	211	225	226	240	241	255	256	270
v.1	CCGGTGAAGTAGCGG	CGCGCGCGCGTCCGC	CTCCCCAAGCCGTT	CCGCACCGCGCGCGC	TCAGCCTCTGCCATG	GCCGGCTCTGGCGCG					
v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
271	285	286	300	301	315	316	330	331	345	346	360
v.1	TGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
v.2	TGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
v.3	TGAAGCGCCTCAAA	TCTATGCTAAGGAAG	GATGATGCGCCGCTG	TTTTTAAATGACACC	AGCGCCTTTGAGTTC	TCGGATGAGGCGGGG					
361	375	376	390	391	405	406	420	421	435	436	450
v.1	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTGGTGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
v.2	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTGGTGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
v.3	GACGAGGGGCTTTCT	CGGTTCAACAAACTT	CGAGTTGTGGTGCC	GATGACGGTTCCGAA	GCCCGGAAAGGCCT	GTTAACGGGGCGGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
v.1	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.2	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					
v.3	CCGACCCCTCCAGGCC	GACGATGATTCCTTA	CTGGACCCAGACTTA	CCTTTGACCAACAGT	CAGCTGAGTTTGAAG	GTGGACTCCTGTGAC					

Figure 4 continued

541	555 556	570 571	585 586	600 601	615 616	630
v.1	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT
v.2	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT
v.3	AACTGCAGCAAAACAG	AGAGAGATACCTGAAG	CAGAGAAAGGTGAAA	GCCAGGTTGACCAATT	GCTGCCGTTCTGTAC	TTGCTTTTCATGATT
631	645 646	660 661	675 676	690 691	705 706	720
v.1	GGAGAACCTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC
v.2	GGAGAACCTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC
v.3	GGAGAACCTGTAGGT	GGATACATTGCAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGCGCCATCATATCTC
721	735 736	750 751	765 766	780 781	795 796	810
v.1	ACCCTGCTTGCCTTG	TGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT
v.2	ACCCTGCTTGCCTTG	TGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT
v.3	ACCCTGCTTGCCTTG	TGCTATCATCAAAA	TCACCAACCAAAAAGA	TTCACCTTTGGATT	CATCGCTTAGAGGTT	TTGTCAGCTATGATT
811	825 826	840 841	855 856	870 871	885 886	900
v.1	AGTGTGCTGTGGTG	TATATACTTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGGAGAT
v.2	AGTGTGCTGTGGTG	TATATACTTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGGAGAT
v.3	AGTGTGCTGTGGTG	TATATACTTTATGGGA	TTCCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGGAGAT
901	915 916	930 931	945 946	960 961	975 976	990
v.1	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACTCCCATTC
v.2	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACTCCCATTC
v.3	ATAATGCTCATCACC	GCAGCTGTTGGAGTT	GCAGTTAATGTAATA	ATGGGGTTTCTGTTG	AACCACTCTGGTCAC	CGTCACTCCCATTC
991	1005 1006	1020 1021	1035 1036	1050 1051	1065 1066	1080
v.1	CACCTCCCTGCCTTCA	AATTCCTCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTGA
v.2	CACCTCCCTGCCTTCA	AATTCCTCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTGA
v.3	CACCTCCCTGCCTTCA	AATTCCTCCCTACCCAGA	GGTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCCTGGCAGTG	AGAGCTGCATTGTGA
1081	1095 1096	1110 1111	1125 1126	1140 1141	1155 1156	1170
v.1	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AGAGATTGCTGAGCCCC
v.2	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AGAGATTGCTGAGCCCC
v.3	CATGCTTTGGGAGAT	TTGGTACAGAGTGT	GGTGTGCTAATAGCT	GCATACATCATACGA	TTCAAGCCAGATAAC	AGAGATTGCTGAGCCCC
1171	1185 1186	1200 1201	1215 1216	1230 1231	1245 1246	1260

Inventor: Pia M. CHALLITA-EID et al.

Title: NUCLEIC ACID AND ENCODED ZINC TRANSPORTER
PROTEIN ENTITLED 108P5H8 USEFUL IN TREATMENT
AND DETECTION OF CANCER

REPLACEMENT SHEET 10/38

Figure 4 continued

v.1	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATATGGGAT	ACAGTAGTTATATA	CTAGAAGGTGTGCCA					
v.2	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATATGGGAT	ACAGTAGTTATATA	CTAGAAGGTGTGCCA					
v.3	ATCTGTACATACGTA	TTTTTCATTACTTGTG	GCTTTTACAACATTT	CGAATCATATATGGGAT	ACAGTAGTTATATA	CTAGAAGGTGTGCCA					
1261	1275	1276	1290	1291	1305	1306	1320	1321	1335	1336	1350
v.1	AGCCATTTTGAATGTA	GACTATATCAAGAA	GCCTTCATGAAAATA	GAAGATGTATATTC	GTGGAAGATTTAAAT	ATCTGCTCTCTCACT					
v.2	AGCCATTTTGAATGTA	GACTATATCAAGAA	GCCTTCATGAAAATA	GAAGATGTATATTC	GTGGAAGATTTAAAT	ATCTGCTCTCTCACT					
v.3	AGCCATTTTGAATGTA	GACTATATCAAGAA	GCCTTCATGAAAATA	GAAGATGTATATTC	GTGGAAGATTTAAAT	ATCTGCTCTCTCACT					
1351	1365	1366	1380	1381	1395	1396	1410	1411	1425	1426	1440
v.1	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAATGG	GAGGAAGTACAGTCC	AAAGCAAAACCATTTA					
v.2	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAATGG	GAGGAAGTACAGTCC	AAAGCAAAACCATTTA					
v.3	TCAGGAAAATCTACT	GCCATAGTTCACATA	CAGCTAATTCCTGGA	AGTTCATCTAATGG	GAGGAAGTACAGTCC	AAAGCAAAACCATTTA					
1441	1455	1456	1470	1471	1485	1486	1500	1501	1515	1516	1530
v.1	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAATTTGTCAGAGT					
v.2	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAATTTGTCAGAGT					
v.3	TTATTGAACACATTT	GGCATGTATAGATGT	ACTATTCAGCTTCAG	AGTTACAGGCAAGAA	GTGGACAGAACTTGT	GCAATTTGTCAGAGT					
1531	1545	1546	1560	1561	1575	1576	1590	1591	1605	1606	1620
v.1	TCTAGTCCCTAATTT	TATGTATT--TTGGG	AACCTCTG--TTTAC	CTTATTTATCTCTGCA	GTCCACAGACTTGAGA	GCAATTAATGCAAAAC					
v.2	TCTAGTCCCTAATTT	TATGTATT--TTGGG	AACCTCTG--TTTAC	CTTATTTATCTCTGCA	GTCCACAGACTTGAGA	GCAATTAATGCAAAAC					
v.3	TCTAGTCCCTAATTT	TATGTATTGTTTATG	CATTCTGATTTTAC	TTTATTTATCTCTGCA	GTCCACAGACTTGAGA	GCAATTAATGCAAAAC					
1621	1635	1636	1650	1651	1665	1666	1680	1681	1695	1696	1710
v.1	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCTGATCAAGC	ATCAGTCTCTCAAAAC	AGTTGCCCCAGCCTG	ACAGTGTAGTCTCT					
v.2	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCTGATCAAGC	ATCAGTCTCTCAAAAC	AGTTGCCCCAGCCTG	ACAGTGTAGTCTCT					
v.3	CTAAATGAGAAAATG	GAATCCCTGACAGCT	GTGTCCTGATCAAGC	ATCAGTCTCTCAAAAC	AGTTGCCCCAGCCTG	ACAGTGTAGTCTCT					
1711	1725	1726	1740	1741	1755	1756	1770	1771	1785	1786	1800
v.1	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v.2	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTC-TACAGAT					
v.3	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	GTTTCCCAAAACACTG	TTTACAGAATGAGAT	GTGACTCCTACAGAT					
1801	1815	1816	1830	1831	1845	1846	1860	1861	1875	1876	1890

Figure 4 continued

v.1	ACCTCATAGAAGACA	ATCCAAGATCATACT	TCATTAACCTTGACAG	AGTACGTGCTCTTAA	GGAAGCATCAAGAAT	TCAATATTTGCATTT
v.2	ACCTCATAG-----	-----	-----	-----	-----	-----
v.3	ACCTCATAG-----	-----	-----	-----	-----	-----
1891	1905 1906	1920 1921	1935 1936	1950 1951	1965 1966	1980
v.1	AAAAATACCTTTTAA	GGCCATTTTATATTA	AGCCAGTGTGGAAA	ACTGAATTTTTTTTA	TTATGTATATAATC	TCGACACCCAGCTTC
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
1981	1995 1996	2010 2011	2025 2026	2040 2041	2055 2056	2070
v.1	TGGAATTGCTGCTTT	CTTTTACAGAAAT	ACTACCCACAGATT	TCAGGAAGTACTAGT	AGTTATCCCAAAAGT	GGATAAGCATGTAT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2071	2085 2086	2100 2101	2115 2116	2130 2131	2145 2146	2160
v.1	TCCTAAGTGTTCAG	AAATGTTTATTTCA	CACATAAGTCTTAAAT	GTTATTGTTATGATT	ATACTTTATAAACAA	CCTTTCCAGATGCT
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2161	2175 2176	2190 2191	2205 2206	2220 2221	2235 2236	2250
v.1	ACAGGGTTTTGAATC	TCAAAGTTAACATTT	TTCATTATTGTAAAT	CITAGAACCAAAATCT	TTATTTATTGTGGTC	ACTGTTATTAATGA
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2251	2265 2266	2280 2281	2295 2296	2310 2311	2325 2326	2340
v.1	TTTAGGAAATACTTT	CAATATTATCTGAA	TGGCTGAAGTTAGTC	TTAAACTCAAATTAC	TATATGATGATTAA	AACAAAATAAAGAG
v.2	-----	-----	-----	-----	-----	-----
v.3	-----	-----	-----	-----	-----	-----
2341	2355 2356	2370				
v.1	CGAGGATGGGAAAA	AAAAAATAAAAAA	AAA	2364		
v.2	-----	-----	---	1548		
v.3	-----	-----	---	1557		